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Db	1187	TCCAGGCCCCCAACACACAGTACGTCTCGGTCAACGACGCGAGCTACTGAGAGTCTGG	1246
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Qy	1021	agctcagccccgggctctggaaagcctccgaagtccgggtccggtcgtcgaagncaaaggttla	1080
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DEFINITION	Homo sapiens	DRC3 mRNA, complete cds.			
ACCESSION	AF282167				
VERSION	AF282167.1	GI:9944939			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 1829) Wu, K., Xu, Z., Wang, M., Xu, X., Han, Y., Cao, Y., Wang, R., Sun, Y. and Wu, M.				
TITLE	Cloning and expression analyses of down-regulated cDNA C6-2a in human esophageal cancer				
JOURNAL	Chung-Hua I Hsueh I Chuan Hsueh Tsa Chih 16 (5), 325-327 (1999)				
MEDLINE	99445952				
PUBMED	10514543				
REFERENCE	2 (bases 1 to 1829)				
AUTHORS	Wang, M., Chen, B., Wu, K., Xu, X., Han, Y., Cai, Y., Wang, J., Xu, Z. and Wu, M.				
TITLE	Direct Submission				
JOURNAL	Submitted (26-JUN-2000) National Laboratory of Molecular Oncology, Cancer Institute, CAMS, PUMC, Panjiayuan, Chaoyang Qu, Beijing 100021, China				
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 ACCESSION BC004907  
 VERSION BC004907.1 GI:13436193  
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 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 2169)  
 Strausberg, R.  
 Direct Submission  
 Submitted (21-MAR-2001) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Rudin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
 DNA Sequencing by: Institute for Systems Biology  
<http://www.systemsbio.org>  
 contact: amadan@systemsbio.org  
 Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia  
 Greene, Mark Kettelman and Anuradha Madan

REMARK  
 COMMENT  
 Clone distribution: MGC clone distribution information can be found  
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VERSION AC019238.5
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 204340)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 204340)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (30-DEC-1999) Genome Sequencing Center, Washington
REFERENCE University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Aug 17, 2000 this sequence version replaced gi:9280808.

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----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0700B05
----- Summary Statistics -----
Sequencing vector: M13; 848
Sequencing vector: plasmid; 16%
Chemistry: Dye-terminator Big Dye; 16% of reads
Chemistry: Dye-terminator Big Dye; 16% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 199676 bases at least Q40
Consensus quality: 200928 bases at least Q30
Consensus quality: 201749 bases at least Q20
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Insert size: 204523; sum-of-contigs
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Quality coverage: 7.57 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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2853 5901: contig of 3049 bp in length
5902 6001: gap of unknown length
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12966 13065: gap of unknown length
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21019 21119: gap of unknown length
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95162 95261: gap of unknown length
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DEFINITION	Homo sapiens DR3 gene, complete cds.		PRI
ACCESSION	AF282168		
VERSION	AF282168.1	GI:9944941	
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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	Wu,K., Xu,Z., Wang,M., Xu,X., Han,Y., Cao,Y., Wang,R., Sun,Y. and Wu,M.		
TITLE	Cloning and expression analyses of down-regulated cDNA C6-2A in human esophageal cancer		
JOURNAL	Chung-Hua I Hsueh I Chuan Hsueh Tsa Chih 16 (5), 325-327 (1999)		
MEDLINE	99445952		
PUBMED	10514543		
REFERENCE	2 (bases 1 to 5985)		
AUTHORS	Wang,M., Chen,B., Wu,K., Xu,X., Han,Y., Cai,Y., Wang,J., Xu,Z. and Wu,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (26-JUN-2000) National Laboratory of Molecular Oncology/Cancer Institute, CAMS, PUMC, Panjiyuan, Chaoyang Qu, Beijing 100021, China		
FEATURES	Location/Qualifiers		
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 2646)		
JOURNAL	Strausberg, R.		
REMARK	Direct Submission		
COMMENT	Submitted (05-FEB-2001) National Institutes of Health, Mammalian		
	Gene Collection (MGC), Cancer Genomics Office, National Cancer		
	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,		
	USA		
	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>		
	Contact: Robert Strausberg, Ph.D.		
	Tel: (301) 496-1550		
	Email: <a href="mailto:Robert.Strausberg@nih.gov">Robert.Strausberg@nih.gov</a>		
	Tissue Procurement: DCD/DTP		
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	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
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REFERENCE	TITLE	JOURNAL
1 (sites)		
Watanabe, K., Kumagai, A., Iekura, S., Yamazaki, M., Tashiro, H., Oca, T., Suzuki, Y., Odayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Nakamura, Y., Isogai, T. and Sugano, S.	NEDO human cDNA sequencing project	Unpublished (2000)

**REFERENCE**  
2 (bases 1 to 3074)  
Sugano, S., Suzuki, Y., Ota, T., Ohashi, M., Nishi, T., Isogai, T.,  
Shibahara, T., Tanaka, T. and Nakamura, Y.  
**TITLE**  
Direct Submission  
**JOURNAL**  
Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sumitomo

Sugano, Institute of Medical Science, University of Tokyo,  
Laboratory of Genome Structure Analysis, Human Genome Center;  
Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan  
(E-mail: cdna@elms.u-tokyo.ac.jp, tel: 81-3-5449-5286,  
fax: 81-3-5449-5416)

COMMENT  
NEO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan: cDNA full insert sequencing: Research Association for Biotechnology: cDNA library construction, 5'- & 3'-end one pass sequencing: Department of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).

FEATURES	Location/Qualifiers
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 DEFINITION Mus musculus, similar to hypothetical protein FLJ21935, clone  
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 VERSION BC005492.1 GI:13529553  
 KEYWORDS MGC.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 3079)  
 AUTHORS Strausberg, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (27-MAR-2001) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
 REMARK  
 COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: [Robert.Strausberg@nih.gov](mailto:Robert.Strausberg@nih.gov)  
 Tissue Procurement: Lohar Hennighausen Ph.D., Robin Humphreys  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
 DNA Sequencing by: Sequencing group at the Stanford Human  
 Genome Center, Stanford University School of Medicine, Stanford, CA 94305  
 Web site: <http://www.shgc.stanford.edu>  
 Contact: (Dickson, Mark) [mdickpaxil@stanford.edu](mailto:mdickpaxil@stanford.edu)  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.  
 Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>  
 Series: IRAK Plate: 7 Row: 1 Column: 23.

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DEFINITION Homo sapiens chromosome 19 clone CTC-550B14, WORKING DRAFT
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SEQUENCE 11 ordered pieces.
AC011476.6 GI:9256296
AC011476.6
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 188302)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 19
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 188302)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Subcloning
JOURNAL Submitted (07-OCT-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94596, USA
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COMMENT
On Jul 18, 2000 this sequence version replaced gi:8576068.
-----Genome Center
Center: Joint Genome Institute
Center code: JGI
Web site: http://www.jgi.doe.gov
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Project Information
Center Project Name: 396418, BC361442
Center clone name: CIT-HSPC_550B14
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Summary Statistics
Consensus quality: 185362 bases at least Q40
Consensus quality: 185327 bases at least Q30
Consensus quality: 186988 bases at least Q20
Estimated insert size: 189730; agarose-IP estimation
Estimated insert size: 187852; sum-of-ctdigs estimation
Quality coverage: 8.28 in Q20 bases; agarose-IP estimation
Quality coverage: 8.36 in Q20 bases; sum-of-ctdigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1 19837: contig of 19837 bp in length
19838 19937: gap of unknown length in length
19938 66572: contig of 46635 bp in length
66573 66573: gap of unknown length
66573 69024: contig of 2352 bp in length
69025 69125: gap of unknown length
69125 81795: contig of 12670 bp in length
81795 81895: gap of unknown length
81895 88331: contig of 6437 bp in length
88331 88332: gap of unknown length
88332 94151: contig of 5720 bp in length
94151 94152: gap of unknown length
94152 147534: contig of 53283 bp in length
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* 125628 148303: contig of 22576 bp in length
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* 148304 174330: contig of 26027 bp in length
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FEATURES

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Job time: 6483 sec

Fri Jun 29 08:51:07 2001

us-09-717-883a-1.rge

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Page 18



PT	reflects relative abundance of corresp. mRNA in specific human
PT	tissues
XX	Claim 1; Page 1154; 2245bp; Japanese.
PS	
CC	A single-stranded DNA (or its complementary strand or the corresp.
CC	double-stranded DNA) which comprises one of the 7837 "GS" sequences
CC	given in AAT19001-T26837 and which is able to hybridise to part of
CC	human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
CC	sequences were obtained from 3'-directed cDNA libraries prepared
CC	from various human tissues; synthesis of cDNA was initiated from the
CC	3'-end of mRNA by using poly(7) as the sole primer. Since the 3'-
CC	untranslated sequence is unique to a particular mRNA species, almost
CC	all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
CC	is constructed so as to reflect accurately the relative abundance of
CC	different mRNAs in the particular tissue from which it was derived.
CC	The appearance frequency of a given GS in a cDNA library can be
CC	determined (esp. using primers and probes derived from the GS
CC	sequences) as a means of diagnosing abnormal cell function or for
CC	recognising different cell types.
CC	
SQ	Sequence 134 BP; 32 A; 31 C; 47 G; 23 T; 1 other;
QY	
QY	Query Match 7.8%; Score 127.8; DB 16; Length 134;
QY	Best Local Similarity 97.7%; Pred. No. 5,7e-18;
QY	Matches 129; Conservative 0; Mismatches 3; Indels 0; Gaps
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Db	1 gactctgactgctgctggagtgaggagggcgctggagacagcttaaggaagcgctanagga 60
QY	1542 cccccagagaggctgcagcttgagacccctgagcatctgtaatatcgggccagcctataaacag 1601
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Db	121 cctccgctgctta 132
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AC	AA295379;
XX	
DT	01-JUN-2000 (first entry)
XX	
DE	Human colon specific gene (CSG) SEQ ID NO:1.
XX	
KW	Human; colon specific gene; CSG; diagnosis; colon cancer; detection;
KW	cytostatic; ds.
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OS	
XX	MO200007632-AL.
PN	17-FEB-2000.
PD	
XX	20-JUL-1999; 99WO-US16357.
PF	
XX	04-AUG-1998; 98US-0095231.
PR	
XX	
XX	(DIAD-) DIADEXUS LLC.
PA	
XX	Sun Y, Recipon H, Macina RA;
XX	
DR	WPI; 2000-205579/18.
PT	
PT	Novel methods for diagnosing, monitoring, staging, imaging and treating
PT	colon cancer by measuring the level of colon specific gene markers -

PS Claim 6: Page 37-38: 42pp: English.

XX The present invention describes a method for diagnosing the presence of  
CC colon cancer in a patient. The method comprises measuring levels of  
CC colon specific gene markers (CSG) in cells, tissues or bodily fluids,  
CC and comparing the measured levels of CSG with levels of CSG from a  
CC normal human control, where an increase in measured CSG levels in the  
CC patient versus control is associated with the presence of colon cancer.  
CC AA295379 to AA295381 represent human CSG sequences. The method is used  
CC to detect, monitor, stage or give a prognosis for colon cancer.  
CC Antibodies against CSGs are used for detection or image localisation of  
CC the CSGs. The antibodies can be conjugated to cytotoxic agent or drug and  
CC used to treat colon cancer. The method of the invention is more accurate  
CC than prior art clinical methods for staging colon cancer, because it  
CC measures colon specific markers, and, unlike pathological staging  
CC methods, do not depend on an invasive procedure.

XX Sequence 1710 BP: 437 A; 529 C; 444 G; 299 T; 1 other:

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Matches 336; Conservative 0; Mismatches 338; Indels 10; Gaps 3;

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OY 305 aacgagctctggaactcgtctggggaactcgttgacccgcccgggctctgagctctcccg 364
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OY 539 cgaagatctgagcctcagctg--gagtcagagacagcaggaanaatgggtccctgtaact 594
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DB 911 cccaactcagagcctctccagcccaaacctgcccagccgagccttgaataatgactcttg 970
OY 595 tatgacttcagagcccgcaacagcagctgctgctgctgaagcagcgagcagctactgag 654
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DB 971 tagcggtctgaaagctagagccacacagcagctgactgctgctcagggagagagagctg 1030
OY 655 gcccggagatgacagcgtatagtggtggagaggttcggagccagcggggagagagagat 714
    || || || || || || || || || || || || || || || || || || || || ||
DB 1031 gtctcggagacacagcagcgctgctgctgctgagaaatgagagcgagcagcgctac 1090
OY 715 gtgcctacacacatcctgacaccc 738
    || || || || || || || || || || || || || || || || || || || || ||
DB 1091 attccaaagacacatcctctggagccc 1114

```

RESULT 4  
AAF32641

ID AAF32641 standard: cDNA: 2220 BP.

XX AAF32641:

DT 22-MAR-2001 (first entry)

DE Human cDNA encoding intracellular signalling molecule INTRA4.

XX Human, intracellular signalling molecule: INTRA; immunosuppressive;  
KM cytosolic; neuroprotective; neurotropic; antiarteriosclerotic; cancer;  
KM antiinflammatory; anti-HIV; neuroleptic; antibacterial; antifungal;  
KM antiviral; antiparasitic; antihelminthic; antiparkinsonian; AIDS;  
KM cell proliferative disorder; arteriosclerosis autoimmune; epilepsy;  
KM inflammatory disorder; Addison's disease; gastrointestinal disorder;  
KM neurological disorder; Parkinson's disease; Creutzfeldt-Jakob disease;  
KM mental disorder; schizophrenia; anxiety; ss.

XX Homo sapiens.

XX WO200077040-A2.

XX 21-DEC-2000.

XX 16-JUN-2000; 2000WO-US16636.

XX 16-JUN-1999; 99US-0139566.

XX 17-AUG-1999; 99US-0149640.

XX 09-NOV-1999; 99US-0104417.

XX (INCY-) INCYTE GENOMICS INC.

XX Yue H, Tang YT, Hillman JL, Lal P, Bandman O, Baughn MR;  
PI Azimzal Y, Yang J, Reddy R, Lu DM;

XX WPI: 2001-025334/03.

XX P-PSDB: AAB64372.

XX New human intracellular signalling molecules, useful for the diagnosis,  
PT prevention and treatment of cell proliferative, autoimmune,  
PT inflammatory, neurological, gastrointestinal, reproductive and  
PT developmental disorders -

PS Claim 5: Page 162; 192pp: English.

XX Sequences AAF32638 - AAF32689 represent cDNA encoding human  
CC intracellular signalling molecules INTRA1 - INTRA52, represented in  
CC AAB64369 - AAB64420. Modulators of the intracellular signalling molecules  
CC of the invention exhibit immunosuppressive; cytosolic; neuroprotective;  
CC neurotropic; antiarteriosclerotic; antiinflammatory; anti-HIV;  
CC neuroleptic; antibacterial; antifungal; antiviral; antiparasitic;  
CC antihelminthic; and antiparkinsonian activity. INTRA polypeptides their  
CC agonists and antagonists are useful for the treatment of a condition  
CC associated with decreased or increased expression of functional INTRA.  
CC Disorders associated with abnormal INTRA expression or activity include  
CC cell proliferative disorders e.g. arteriosclerosis and cancers;  
CC autoimmune or inflammatory disorders e.g. Addison's disease and acquired  
CC immunodeficiency syndrome (AIDS); viral, bacterial, fungal, parasitic,  
CC protozoal and helminthic infections; gastrointestinal disorders e.g.  
CC dysphagia and irritable bowel syndrome; neurological disorders e.g.  
CC epilepsy and Parkinson's disease; prion diseases e.g. Creutzfeldt-Jakob  
CC disease and mental disorders e.g. anxiety, schizophrenia and Tourette's  
CC disorder. Antibodies immuno specific for the INTRA proteins may also be  
CC useful in the diagnosis of the above disorders.

XX Sequence 2220 BP: 549 A; 696 C; 593 G; 382 T; 0 other:

Query Match 5.7%; Score 93.2; DB 22: Length 2220;  
Best Local Similarity 49.1%; Pred. No. 1.3e-10;  
Matches 336; Conservative 0; Mismatches 338; Indels 10; Gaps 3;

```

OY 65 cccctggagagccaggtacacgacgtgctgcagaagaatgaagtaacgcttcagctgtctg 124
DB 948 cttcacccagggcacagttatctgactgtcttcacgaagatcaagttacagcttcacgtctg 1007
OY 125 gcccgctctgcgggacaacatcgccaccctctctccggaactgtttgaactctcttc 184
DB 1008 ggaaggtctggcgaactgtgctgaagaagaatgccccttgatcgtacatctctcttc 1067
OY 185 gggcctctgcagatgattgtgaacacgttcggggggccgggaattcgcagcagctgtgcg 244
DB 1068 aagtcctgaactcatctcgtgcaggtgctcctgaggctgctagcagcccaagtgtatc 1127
OY 245 cggcgcatctgacatctgagatgcgtgctgcgtcgtcgggaaacgtcaactcaactgaa 304
DB 1128 tcaacctcttcaacccctaaagctatacaacctgtacacgtctctgtcttaagccactgag 1187
OY 305 aacgagctctgacatctgctggtggagctgtgtgaccccgcccggtctgagctgtcccg 364
DB 1188 agtaaccttggatggtgtgggtccagcctggaaccactagccggccgacgtgacaggc 1247
OY 365 gaggagggagccccaacagacagccgagttctcagcggctgaggagccgctgacatgac 424
DB 1248 gatgagccctctgcctacacacccacattctcgtgagtactggaacttccagagccctcc 1307
OY 425 ccgcagagagcgc---gcttgggagagccacgttggagaacagct---acagcagagcgg 478
DB 1308 agccaagacaccttagatagatcacagaccctgttctccttcggggggaagtatagttta 1367
OY 479 aggcgcggcgcaagaagcgcccccgaagtcgctgcaatggtcagcggagagacttggagc 538
DB 1368 gggagacactcaacttctcctgaagagaacacacacatgataccctcagctgtggac 1427
OY 539 cagaatctgagcgtcagctgctgctgctgctgctgctgctgctgctgctgctgctgctg 594
DB 1428 cccaactcagagccctcagcagcccaacactgcccagccagccctgaagaatcgaactctg 1487
OY 595 tatgcttccggagcccgcaacagcagtgagctgtcgtcgaagcagcggagactgagag 654
DB 1488 taagaatttgaagctagaagaacccagggaaactgactgtgtccagggagagaagaagctgag 1547
OY 655 gtccctgagatgacgtcgtgaagtggtggaaggttcgggacccagcggggcagagagagat 714
DB 1548 gtctcgagacacagcaagcggtgtgtgtgtgaagaatgagggcgagagcgagcgtctac 1607
OY 715 gtgcctctacaactctctacacc 738
DB 1608 attccaagcaacatctctgagccc 1631

```

RESULT 5  
AA040730  
ID AA040730 standard; DNA: 3245 BP.

```

AC AA040730;
XX
XX 25-AUG-1993 (first entry)
XX
XX Mouse eps8.
XX
XX Epidermal growth factor receptor; EGFR-pathway substrate; eps;
XX tyrosine kinase receptor; TKR; SH2; SH3; mitogenesis; ss.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX CDS 246..2711
XX FT /*tag= a
XX FT polyA_signal 3036..3041
XX FT /*tag= b
XX
XX US7935311-A.
XX
XX 01-APR-1993.

```

```

XX XX
XX 25-AUG-1992; 92US-0935311.
XX PF
XX 25-AUG-1992; 92US-0935311.
XX PR
XX (USSH ) US DEPT HEALTH & HUMAN SERVICE.
XX PA
XX DI Fiore PP, Fazioli F;
XX PI
XX WPI: 1993-159477/19.
XX DR P-PSDB: AAR35451.
XX DR
XX Epidermal growth factor receptor substrate, eps 8 - used to
XX PT enhance mitogenic response of cells to epidermal growth factor
XX PS
XX Disclosure; Page 30-34; 40pp; English.
XX CC
XX Eps8 is a novel EGFR substrate. The protein bears the
XX CC characteristic signatures of TKR substrates including SH2 and
XX CC SH3 domains. Eps8 is involved in the transduction of mitogenic
XX CC signals and it can be used to enhance the mitogenic response of
XX CC cells to EGF.
XX
XX Sequence 3245 BP; 885 A; 805 C; 865 G; 690 T; 0 other.

```

Query Match 5.6%; Score 92.2; DB 14; Length 3245;  
Best Local Similarity 51.9%; Pred. No. 2.2e-10;  
Matches 233; Conservative 0; Mismatches 213; Indels 3; Gaps 1;

```

OY 30 ctggggagggctctcagctgcggcgcaagccgcccctggaggcgagtaacagcag 89
DB 1177 ctggagaggggttttaacatcagtgaggaacccgcccacccctcagagattgtgact 1236
OY 90 tgcgcgaagaataagctacgctcagcgtctgctgctggccggctgcgggaacatgcg 149
DB 1237 gtccagaagaatttaacatgattcaacctctcggccaagtgaagttccataccaga 1296
OY 150 acccctctctcggagctgttgactctcttccgggctctcgaatgattgagaca 209
DB 1297 acccgatgctcagatctgttcatcttttgttactcactaataatgtgttcagg 1356
OY 210 cgttcggggggcggaatttcggagcagtggtgcggcgccgcatctacatcgatgcg 269
DB 1357 caaagggtggccctgaactggtccagttcgtgtactcagccactgttgacaagaacag 1416
OY 270 tggcgcgtcgcgagacagctacacgtggaacagagctctgactcgtgtggg 329
DB 1417 ttgatttcttaactacacagccactgtcggaagagaagcgtgtgagtctcactggag 1476
OY 330 actcgtgagcccgcccggtgagctgtcccgagagag---gaaaccccatacagac 386
DB 1477 atagtgtgtagaagtgaagcagagtggtgcgaagaagacagttcatctcaccttaagtc 1536
OY 387 ccgagttctcagcgcgtctggagcggcggtcaactgaccccgagagcggcgctgtgag 446
DB 1537 cgaagttccgaaagcgtgtggagcccccagatgtcgtacattcatggtggcgccacagagc 1596
OY 447 acccagttgaaacagctacagcagag 475
DB 1597 aagacatgtatcaactgtgccgagttccgtg 1625

```

RESULT 6  
AAK53491/C  
ID AAK53491 standard; DNA: 114955 BP.

```

AC AAK53491;
XX
XX 05-JUL-1999 (first entry)
XX
XX Human adenosine A1 receptor antisense oligonucleotide fragment.
XX
XX

```













[illegible][illegible]

PT obtaining agonists and antagonists

Job time: 4112 sec

XX Disclosure: Page 149-160; 285pp; English.

XX  
CC DNA encoding the alpha 1B subunit was isolated by screening a  
CC human basal ganglia cDNA library with fragments of the rabbit  
CC skeletal muscle calcium channel alpha 1 subunit-encoding cDNA.  
CC A portion of one of the positive clones was used to screen an  
CC IMR32 cell cDNA library. Clones that hybridised to the basal  
CC ganglia probe were used to further screen an IMR32 cell cDNA  
CC library to identify overlapping clones that in turn were used  
CC to screen a human hippocampus cDNA library. A series of clones  
CC to span nearly the entire length of the nt. sequence encoding  
CC the human alpha 1B subunit was obt'd. Nucleic acid amplification  
CC of specific regions of the IMR32 cell alpha 1B mRNA yielded  
CC additional segments of the alpha 1B coding sequence. A full-  
CC length alpha 1B DNA clone was constructed by ligating portions  
CC of the partial cDNA clones. Nucleic acid amplification analysis  
CC of IMR32 cell RNA and genomic DNA using oligo primers corresp. to  
CC sequences located 5' and 3' of the stop codon of the DNA encoding  
CC the alpha 1B subunit revealed an alternatively spliced alpha  
CC 1B-encoding mRNA in IMR32 cells. This second mRNA product is the  
CC result of differential splicing of the alpha 1B subunit transcript  
CC to include another exon that is not present in the mRNA corresp.  
CC to the other 3' alpha 1B cDNA sequence that was initially isolated.  
CC The alpha 1B subunit encoded by a DNA sequence contg. an additional  
CC exon is referred to as alpha 1B-1 and given in AA084657/R71005.  
CC Whereas the other form is referred to as alpha 1B-2 and is given in  
CC AA084658/R71006. Following the sequence of the additional exon in  
CC alpha 1B-1 the alpha 1B-1 and alpha 1B-2 sequences are identical.  
XX  
S0 Sequence 7175 BP; 1415 A; 2197 C; 2168 G; 1395 T; 0 other:

Query Match 2.98; Score 46.6; DB 16; Length 7175;

Best Local Similarity 46.7%; Pred. NO. 0.71;

Matches 209; Conservative 0; Mismatches 237; Indels 2; Gaps 2;

OY 855 ggaacgggcccgcgtggaacgtgtgatatnctcaacggcttgaccacgagagag 914  
DB 2748 gcaaggggcccgaagagcgagagcgggagccggctcccggaagagcgccgccc 2807  
OY 915 aaatctccagatgcatcgtcaacaggaactgcagcgcgccctgcccagggccgc 974  
DB 2808 caccgcagcacaagaaagagcgcgccggcccccggagcgcgagcgagcgccga 2867  
OY 975 tcggagacgagcgcgccgacgtcccaaggcccgccgcccgaacgcagctcagccgggc 1034  
DB 2868 ggcacagggcccgaagggcgcgccggcagcaccacggcgcgctcccgagagggcgcc 2927  
OY 1035 tcggagcgtctcganagtccgagcgtgctgcagagcagaaggccttagctccggagcgtg 1094  
DB 2928 gagcgggagggcccgacacggcgcgacggcagcgatccgacgaagaggtgcgcc 2987  
OY 1095 gacgagcgggtgtgtctgacccggggcgacatttctcgtcgtcgaagaaggagagctgcg-9 1153  
DB 2988 ggcgcacaaggcgagcgcgcgcgcgacccggcgcccgcccgagcgggcgccgggag 3047  
OY 1154 gcggtgagcccccgagaggggagcagctgtgtacagcacaaggtcaacgctcagcgcttcgct 1213  
DB 3048 gcgagagagcgaggagagccggcgcgccggcagcgccgacacaagcgcgagcctgtc 3107  
OY 1214 gctgagagacaagaaggtctcagagctcgagagcagtgatgagagagcacaagaagaa 1273  
DB 3108 -cagagagcgtgtgagagagagagacacagagagagagagccacgagagagaggtcagat 3166  
OY 1274 ggtggaagcgaggtcgaatctggaagtc 1301  
DB 3167 agtggagagcgagcagaagagagagctc 3194



...



QY	30	ctgggagagagctctgtcaagctcgcgagccagccgccttcgagagccgagtaaccagcg	89
Db	1177	CTGGAGAGAGGCGGTTTAACTACGTAGGGCAAAACCCGACCCTCTGTACAGATTGTTGACT	12336
QY	90	tgtctcgaagaataagtaacgcttcaagcctctgagccgagctgcgcggaacaatgcgcg	149
Db	1237	GTTTCCAGAAAGTTTAAACATGAGATTTTCAACCTTCGTGCCAAGTTGAAGTCCCATATCCAGA	1296
QY	150	aacccctcctcccgagctgttgacacctcttctggagctcttgaaatgatgtggaaca	209
Db	1297	ACCCGAGTGCCTTCAGATCTGTGTTCAATTTTGTTTACTCCACTAAATATGGGTCCAGG	1356
QY	210	cgtcgggggagccgagcttcgcagcaagltgtggygcgcgcgatctgacatcgatgcg	269
Db	1357	CACAGAGTGCGCCTCGAAGCTGGCCAGTTGGTACTGACCCCATGTTGACAAAAGACAG	1416
QY	270	tggcgctgcgcgcygggagacaagctaacctccacgtgaaagaagctcttgacctctg	329
Db	1417	TTGATTTCTTAAACTAACACAGCCACATCGCGAGGAACGAAGCTGTGATGTCACAGCGAG	1470
QY	330	actcgttgagaccgcgcccgagcttgagagctgtcccgagagag---gagccccaatagac	386
Db	1477	ATATGTTGGGGAAGAAGTAAAGACAGAGATGGCGCCAAAGAAACAGTTCAATCCCACTTTCAGTCC	1536
QY	387	ccgagctcttcacgcgagcttgagagccgcggtcaactgaccccgagagccgcgagct	446
Db	1537	CGAAGTTCGCCAACAGGCTGGGAGCCCCCATGTGTGAATCTTATGGGCGGCCACACAGAGC	1596
QY	447	accagagctgagaaacagctacagcagag	475
Db	1597	AAGACATGTATCAACTGCGCCGAGTCCGCTG	1625

RESULT 2  
 US-08-368-079-3  
 ; Sequence 3, Application US/08368079  
 Patent No. 5610018  
 GENERAL INFORMATION:  
 APPLICANT: DI Fiore, Pier Paolo  
 APPLICANT: Fazioli, Francesca  
 TITLE OF INVENTION: eps8, A Substrate for the Epidermal Growth Factor  
 TITLE OF INVENTION: Kinase, Antibodies Thereeto, and Methods of Use Thereof  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Knobbe, Martens, Olson & Bear  
 STREET: 620 Newport Center Drive, 16th Floor  
 CITY: Newport Beach  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 92660  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/368, 079  
 FILING DATE: 03-JAN-1995  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/935, 311  
 FILING DATE: 25-AUG-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Israelson, Ned A.  
 REGISTRATION NUMBER: 29,655  
 REFERENCE/DOCKET NUMBER: NIN035,001DV1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 235-8550  
 TELEFAX: (619) 235-0176  
 INFORMATION FOR SEQ. ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3245 base pairs  
 TYPE: nucleic acid

```

? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 246..2708
?
US-08-368-079-3

```

Query Match	5.6%;	Score 92.2;	DB 1;	Length 3245;
Best Local Similarity	51.9%;	Pred. No. 11;		
Matches 233;	Conservative 0;	Mismatches 213;	Indels 3;	Gaps
QY 30	cttggagaggtctgtcgtacgctgtgcgggccaagccgcccctcgagagccagataccagacg	89		
Db 1177	CTTGAGAGGGCGCTTTTAAACCTGAGGGCAAAACCGCACCTCTGACAGATTGTGTGACT	12368		
QY 90	tgcctcgagaagatcaagatacgcttaagctctgtcgcccgctgtgcggagcaactcgcgcg	149		
Db 1237	GTTTCCAGAACTTTAAACAACAGATTACACTTCTGGCCAAAGTTGAATCCCATATCCAGA	12366		
QY 150	accocctcccttcgcgagctgtgtgacctcccttcgggaccttcgatatgtatgtgaaca	209		
Db 1297	ACCCGAGTGGTTCAGAACTGGTTCATTTTTGTTTTAACTCAATTAATATGGTGTCAGG	13566		
QY 210	ctgtcgggggggcccggaggtctgcggagaggtgtgcggcgccatctgacatcgtatgcg	269		
Db 1357	CAACAGTGGCCCTGTGAACGTGCCCAAGTTCGGTACTACGCCCACTGTTGACAAAAGACACAG	14166		
QY 270	tggcgctgtctgcgggacaaactactccacgtgaanaacgagctctcgtgacctcgtgcggg	329		
Db 1417	TGTGATTTCCTTAACTATACACAGCCACCTGCGSAGGAACGAGACTGTGAGTGCACCTGGAG	14766		
QY 330	acctcgtgagaccgcccccggtctgtagctctgtccccggagagag---ggaaccccatacagac	386		
Db 1477	ATAGTGGGTGAAAGTGAACGACGAGATGGCCGAAAGAACAGTTCATCCACCTTAACGTCC	15366		
QY 387	ccgagatctctcaagcggctctggagacccgctgcactcagaccccgagagcccgccctggagag	446		
Db 1537	CGAGGTTCCGCAACGGGCTGGGAGCCCCCGATCTGTAACCTTATGGGCGCGGCCACAGACG	15966		
QY 447	accacagttgagaaacagctacagcagag	475		
Db 1597	AAGACATGTTATCAACGCGCGAGTCCGTC	1625		

RESULT 3  
 PCT-US93-07996-3  
 Sequence 3, Application PC/TUS9307996  
 GENERAL INFORMATION:  
 APPLICANT: The Government of the United States, as represented by the  
 APPLICANT: Secretary of Health and Human Services  
 TITLE OF INVENTION: Substrate of the Epidermal Growth Factor Kinase  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Knodbe, Martens, Olson & Bear  
 STREET: 620 Newport Center Drive, 16th Floor  
 CITY: Newport Beach  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 92660  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US93/07996  
 FILING DATE: 19930825  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 235-8550  
 TELEFAX: (619) 235-0176  
 INFORMATION FOR SEQ ID NO: 3:



```

1 MEDIUM TYPE: Diskette
2 COMPUTER: IBM Compatible
3 OPERATING SYSTEM: DOS
4 SOFTWARE: FASTSEQ Version 1.5
5 CURRENT APPLICATION DATA:
6 APPLICATION NUMBER: US/08/455,543A
7 FILING DATE: May 31, 1995
8 PRIOR APPLICATION DATA:
9 APPLICATION NUMBER: 08/223,305
10 FILING DATE: April 4, 1994
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: 07/868,354
13 FILING DATE: April 10, 1992
14 PRIOR APPLICATION DATA:
15 APPLICATION NUMBER: US 07/745,206
16 FILING DATE: 15-AUG-1991
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: US 07/620,250
19 FILING DATE: 30-NOV-1990
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: US 07/482,384
22 FILING DATE: 20-FEB-1990
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: US 07/603,751
25 FILING DATE: 04-APR-1989
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: WO PCT/US89/01408
28 FILING DATE: 04-APR-1989
29 PRIOR APPLICATION DATA:
30 APPLICATION NUMBER: US 07/176,899
31 FILING DATE: 04-APR-1988
32 ATTORNEY/AGENT INFORMATION:
33 NAME: Seidman, Stephanie L.
34 REGISTRATION NUMBER: 33,779
35 REFERENCE/DOCKET NUMBER: 6302-52517
36 TELECOMMUNICATION INFORMATION:
37 TELEPHONE: (619)238-0999
38 TELEFAX: (619)238-0062
39 INFORMATION FOR SEQ ID NO: 8:
40 SEQUENCE CHARACTERISTICS:
41 LENGTH: 7175 base pairs
42 TYPE: nucleic acid
43 STRANDEDNESS: double
44 TOPOLOGY: linear
45 MOLECULE TYPE: DNA (genomic)
46 FEATURE:
47 NAME/KEY: CDS
48 LOCATION: 144..6857
49 FEATURE:
50 NAME/KEY: 5'UTR
51 LOCATION: 1..143
52 FEATURE:
53 NAME/KEY: 3'UTR
54 LOCATION: 6855..7175
55 US-08-455-543A-8

```

Accession	Gene	Protein	Length
OY 1035	tcgaagcctcccgaaatgcacgagcctctgctcagagcaagagagccttaagctcccgagacgctg	1094	
Db 2928	GAGGGGAGACCCCGACGCCACACCGCGGCACACCGGACACAGATCCGACAGAGATGCGCC	2987	
OY 1095	gaacgcgctggtgtgtgtcgtacccgagagcgaactttctcgtcagaagaagagagctcgag-g	1153	
Db 2988	GAGCCCAAGGGCCGACCGCGCCGCGCGCACCCGCGCGCCCGAGCGCGGCCCGCGGAG	3047	
OY 1154	gcggtgagcccccagagagagagcagctgtgtacagccaggtcacccgttcagagcttcgct	1213	
Db 3048	GCGGAGAGCGGGGAGAGGAGCGCGCGCGCGGCACACCGGCCCGCCGACAGGCCAGCTCTCT	3107	
OY 1214	gctgagaggaacaagaagaatgtctcagagcttgagagcagttgatgtgagaaagcaaaagaaga	1273	
Db 3108	-CAcGAGGCTGTGTGAGAGACGACGACACCGGAGAGGAGCGCCACGAGGAAGAGAGCTGAT	3166	
OY 1274	ggtgagagagcaggtgagaaatgtagtctc	1301	
Db 3167	AGTGAAGCCGACACGAAAAAGAGACTTC	3194	

```

1 RESULT 6
2 US-08-193-078B-8
3 : Sequence 8, Application US/08193078B
4 : Patent No. 5846757
5 :
6 : GENERAL INFORMATION:
7 : APPLICANT: Harpold, Michael
8 : APPLICANT: Ellis, Steven
9 : APPLICANT: Williams, Mark
10 : APPLICANT: Feldman, Daniel
11 : APPLICANT: Moeue, Ann
12 :
13 : TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
14 : TITLE OF INVENTION: METHODS
15 :
16 : NUMBER OF SEQUENCES: 29
17 :
18 : CORRESPONDENCE ADDRESS:
19 : ADDRESSEE: BROWN, MARTIN, HALLER & MCCLAIN
20 : STREET: 1660 UNION STREET
21 : CITY: SAN DIEGO
22 :
23 : STATE: CA
24 :
25 : COUNTRY: USA
26 :
27 : ZIP: 92101
28 :
29 : COMPUTER READABLE FORM:
30 : MEDIUM TYPE: Floppy disk
31 :
32 : COMPUTER: IBM PC compatible
33 :
34 : OPERATING SYSTEM: PC-DOS/MS-DOS
35 :
36 : SOFTWARE: Patenlin Release #1.0, Version #1.25
37 :
38 : CURRENT APPLICATION DATA:
39 : APPLICATION NUMBER: US/08/193,078B
40 : FILING DATE: 07-FEB-1994
41 : CLASSIFICATION: 435
42 :
43 : PRIOR APPLICATION DATA:
44 : APPLICATION NUMBER: US 07/868,354
45 : FILING DATE: 10-APR-1992
46 :
47 : PRIOR APPLICATION DATA:
48 : APPLICATION NUMBER: US 07/745,206
49 : FILING DATE: 15-AUG-1991
50 :
51 : ATTORNEY/AGENT INFORMATION:
52 : NAME: Seidman, Stephanie L.
53 : REGISTRATION NUMBER: 33,779
54 : REFERENCE/DOCKET NUMBER: 6362-53607
55 : TELECOMMUNICATION INFORMATION:
56 : TELEPHONE: 619-238-0999
57 : TELEFAX: 619-238-0062
58 :
59 : INFORMATION FOR SEQ ID NO: 8:
60 :
61 : SEQUENCE CHARACTERISTICS:
62 : LENGTH: 7175 base pairs
63 : TYPE: nucleic acid
64 : STRANDEDNESS: double
65 : TOPOLOGY: linear
66 :
67 : MOLECULE TYPE: DNA (genomic)
68 :
69 : FEATURE:
70 : NAME/KEY: CDS
71 :

```

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: LOCATION: 144..6857
: FEATURE:
: NAME/KEY: 5'UTR
: LOCATION: 1..143
: FEATURE:
: NAME/KEY: 3'UTR
: LOCATION: 6855..7175
: US-08-193-078B-8

```

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Query Match 2.9% Score 46.6; DB 2; Length 7175;
Best Local Similarity 46.7%; Pred. No. 0.16;
Matches 209; Conservative 0; Mismatches 237; Indels 2; Gaps 2;

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Oy 855 ggaacagagccgctggaagacgtgcatacancacaggtctgaaccccgagagaagag 914
Db 2748 GCAGACGCCCGCAAGAGCGGAGAGCGGAGCGCGGTCCCGGAGAGCGCGCGCGCG
Oy 915 aaattctccagatgtcatcgtcaacgaagaaactgcaagcgagctggcccaaggcgcg 974
Db 2808 CACCCGACGACAGAGAGAGCGCGCGCGCGCGCGCGCGCGAGAGCGAGCGCGCGCA 2867
Oy 975 tcggagacgagcgagcgagctcccaagcgcccgcccggaacgagctcagccggagc 1034
Db 2868 GGCACAGCGCCCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2927
Oy 1035 tcggagacgctccgagngtccgagcgtgctgagncagaggtcttagctccggagacgtg 1094
Db 2928 GAGCGGAGAGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2987
Oy 1095 gaacgagctgggtgtgtctgaacgagcgagcatttctcgtctgagaagaagagagctgcg-g 1153
Db 2988 GCGCGCAAGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 3047
Oy 1154 ggggagagagcccgagagagagagagagtggtgtatcagcagagtgacagctgagcgcttcgct 1213
Db 3048 GCGGAGAGCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGT 3107
Oy 1214 gctgagagcaagaagaaggtgtcagagcttgagagcagtgatcgaggaagaagaagaaga 1273
Db 3108 -CACGAGCGCTGTGAGACAGACACCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 3166
Oy 1274 ggtggaagcgaggtggaagagtgatc 1301
Db 3167 ACTGCAAGCGCGAGCAAGAAAGAGAGCTC 3194

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RESULT 7
US-08-223-305C-8
; Sequence 8, Application US/08223305C
; Patent No. 5851824
; GENERAL INFORMATION:

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: APPLICANT: Harpold, Michael
: APPLICANT: Ellis, Steven
: APPLICANT: Williams, Mark
: APPLICANT: Feldman, Daniel
: APPLICANT: McCue, Ann
: APPLICANT: Brenner, Robert
: TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
: TITLE OF INVENTION: METHODS
: NUMBER OF SEQUENCES: 57
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Brown, Martin, Haller & McClain
: STREET: 1660 Union Street
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92101-2926
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ Version 1.5

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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/223.305C
: FILING DATE: April 4, 1994
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: 07/868,354
: FILING DATE: April 10, 1992
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 07/745,206
: FILING DATE: 15-AUG-1991
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 07/620,250
: FILING DATE: 30-NOV-1990
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 07/482,384
: FILING DATE: 20-FEB-1990
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 07/603,751
: FILING DATE: 04-APR-1989
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: WO PCT/US89/01408
: FILING DATE: 04-APR-1989
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 07/176,899
: FILING DATE: 04-APR-1988
: ATTORNEY/AGENT INFORMATION:
: NAME: Seidman, Stephanie L.
: REGISTRATION NUMBER: 33,779
: REFERENCE/DOCKET NUMBER: 52516 (P519739)
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619)238-0999
: TELEFAX: (619)238-0062
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 7175 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 144..6857
: NAME/KEY: 5'UTR
: LOCATION: 1..143
: FEATURE:
: NAME/KEY: 3'UTR
: LOCATION: 6855..7175
: US-08-223-305C-8

```

```

Query Match 2.9% Score 46.6; DB 2; Length 7175;
Best Local Similarity 46.7%; Pred. No. 0.16;
Matches 209; Conservative 0; Mismatches 237; Indels 2; Gaps 2;

```

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Oy 855 ggaacagagccgctggaagacgtgcatacancacaggtctgaaccccgagagaagag 914
Db 2748 GCAGAGCGCCCGAAGAGCGGAGAGCGGAGCGCGGTCCCGGAGAGCGCGCGCGCGCG
Oy 915 aaattctccagatgtcatcgtcaacgaagaaactgcaagcgagctggcccaaggcgcg 974
Db 2808 CACCCGACGACAGAGAGAGCGCGCGCGCGCGCGCGCGCGAGAGCGAGCGCGCGCA 2867
Oy 975 tcggagacgagcgagcgagctcccaagcgcccgcccggaacgagctcagccggagc 1034
Db 2868 GGCACAGCGCCCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2927
Oy 1035 tcggagacgctccgagngtccgagcgtgctgagncagaggtcttagctccggagacgtg 1094
Db 2928 GAGCGGAGAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2987
Oy 1095 gaacgagctgggtgtgtctgaacgagcgagcatttctcgtctgagaagaagagagctgcg-g 1153
Db 2988 GCGCGCAAGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGAG 3047

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Oy 1154 gctgtgagcccccagagagggcagctgtgtacagccaggtcaccgtgcagcgttcgct 1213
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Db 3048 GCGGAGAGCGGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 3107
Oy 1214 gctgtgagcaacaagaagtgctcagagctgtgagggcagtgatgaggaagcaaaaga 1273
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3108 -CACGAGCGCTGTGGAGAAAGAGAACCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAT 3166
Oy 1274 gctgtgagcgagcagctgtgaaatgtgagctc 1301
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3167 AGTGAAGCGCGACAAAGAAAGAGAGCTC 3194

RESULT 8
US-08-149-097D-8
; Sequence 8, Application US/08149097D
; Patent No. 5874236
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/149,097D
; FILING DATE: 05-NOV-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/105,536
; FILING DATE: 11-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: MO PCT/US92/06903
; FILING DATE: 14-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/914,231
; FILING DATE: 13-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/868,354
; FILING DATE: 10-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899

```

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; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-55038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 238-0999
; TELEFAX: (619) 238-0062
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7175 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 144..6857
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..143
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 6855..7175
; US-08-149-097D-8

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Query Match 2.9%; Score 46.6; DB 2; Length 7175;
Best Local Similarity 46.7%; Pred. No. 0.16; Mismatches 237; Indels 2; Gaps 2;
Matches 209; Conservative 0;

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Oy 855 ggaacagcccccgtgtgagacagctgcgatanctcaagcgttggaccccccagagaagag 914
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Db 2748 GCAGAGGCGCCGAGAGCGGAGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 2807
Oy 915 aaattctccagatgctatgtcaacgagaatgtcagcgcgcttgcagagcgccg 974
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2808 CACCGACGCCACAGCAGAGAGAGCGCGGCGCGCGCGCGCGCGCGCGAGCGCGCGGA 2867
Oy 975 tcggagccgagcgcgcgcagctcccaagcgcccgagcccgagccagcccgagc 1034
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2868 GCGCCAGGCGCCGAGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2927
Oy 1035 tcgagcgctcgcgagctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1094
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2928 GAGCGGAGCGCCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2987
Oy 1095 gacgcgctggtgtgtgacgcgagcgagcgttcttcgtcagaagaagagctgcg-g 1153
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2988 GCGCCAGAGGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3047
Oy 1154 gctgtgagcccccagagagggcagctgtgtacagccaggtcaccgtgcagcgttcgct 1213
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3048 GCGGAGAGCGGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 3107
Oy 1214 gctgtgagcaacaagaagtgctcagagctgtgagggcagtgatgaggaagcaaaaga 1273
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3108 -CACGAGCGCTGTGGAGAGAGAGAACCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAT 3166
Oy 1274 gctgtgagcgagcagctgtgaaatgtgagctc 1301
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3167 AGTGAAGCGCGACAAAGAAAGAGAGCTC 3194

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RESULT 9
US-08-949-386-8
; Sequence 8, Application US/08949386
; Patent No. 6090623
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: McCue, Ann

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1 APPLICATION NUMBER: 08/105,536
2 FILING DATE: 11-AUG-1993
3 PRIOR APPLICATION DATA:
4 APPLICATION NUMBER: 07/914,231
5 FILING DATE: 13-JULY-1992
6 PRIOR APPLICATION DATA:
7 APPLICATION NUMBER: 07/868,354
8 FILING DATE: 10-APR-1992
9 PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: PCT/US92/06903
11 FILING DATE: 14-AUG-1992
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER: 07/745,206
14 FILING DATE: 15-AUG-1991
15 PRIOR APPLICATION DATA:
16 APPLICATION NUMBER: 07/620,250
17 FILING DATE: 30-NOV-1990
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: 07/603,751
20 FILING DATE: 08-NOV-1990
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: 07/482,384
23 FILING DATE: 02-FEB-1990
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: PCT/US89/01408
26 FILING DATE: 04-APR-1989
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: 07/176,899
29 FILING DATE: 04-APR-1988
30 ATTORNEY/AGENT INFORMATION:
31 NAME: Seidman, Stephanie L.
32 REGISTRATION NUMBER: 33,779
33 REFERENCE/DOCKET NUMBER: 6362-519812
34 TELECOMMUNICATION INFORMATION:
35 TELEPHONE: (619) 238-0999
36 TELEFAX: (619) 238-0062
37 INFORMATION FOR SEQ ID NO: 8:
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 7175 base pairs
40 TYPE: nucleic acid
41 STRANDEDNESS: double
42 TOPOLOGY: linear
43 MOLECULE TYPE: DNA (genomic)
44 FEATURE:
45 NAME/KEY: CDS
46 LOCATION: 144..6857
47 FEATURE:
48 NAME/KEY: 5'UTR
49 LOCATION: 1..143
50 FEATURE:
51 NAME/KEY: 3'UTR
52 LOCATION: 6855..7175
53
54 US-08-450-562-8

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Query Match	2.9%	Score 46.6	DB 3	Length 7175
Best Local Similarity	46.7%	Pred. No. 0.16		
Matches	209	Conservative	0	Mismatches 237; Indels 2; Gaps 2
QY 855	ggaacagagccgcccgtcgagacagctcgtatancctaacagcgttggaccccacgagaagag			914
Db 2748	gcacagagcccccgaamagccgagagccggagcccgctggctccgggaagacggcgccggccg			2807
QY 915	aaatctccacgaatgctcatcgtcaacagaaactgcagcgcgcccttgcgcccagagggcgc			974
Db 2808	caccgcacaccacacacmaagagggcccgccggcccccgcggagggcccggaagagagccggcgga			2867
QY 975	tcggagaccgagccgcgcgcatctccaaagcgcccgccgcggccgaacgcgagctcaagccgggc			1034
Db 2868	ggcccaagcccccgagggcgccggcgccgacacacccggcgccggctcccggagagagccggcc			2927
QY 1035	tcggagcgcttcgaaagtccgcgcctcgtgtgtcgaagmcaagggcgttagcttcggagacgtg			1094

Db	2928	GAGGGGAGCCCGACGCCACCGGCGCAACGGACACAGATCCGACGCAAGAGATGCCCC	2987
Qy	1095	gaagcgctgggtgtgtcgtgacacgggagcgcaactttcttcgtcagaagaagagctgcg-g	1153
Db	2988	GGCCCCAAGGAGCGAGCGCGCCCGCGGCGCACCGCGGGCGGCCCGGAGCGGGGCGGAG	3047
Qy	1154	ggcgtgagcccgccagagagagagcgcaagtgtctacagccagytcaacggttcagcgttcgtc	1213
Db	3048	GGGAGAGCGGGGGAGGAGCGCGCGCGGCGCACCGGGCGCCGGGACAAAGCCAGCCTCCT	3107
Qy	1214	gctggagagcaaaagagaagatgttcagagcttggagcagtgatlgaggaagcaaaagaagaa	1273
Db	3108	-CACGAGGCGTGTGAGAGAGAGGCCACCGAGAGAGAGGAGCGCCACGAGGAAGAGCGCTGAGAT	3166
Qy	1274	ggtggaagcgaggtggaaatggaagtctc	1301
Db	3167	AGTGAAGCGCAGCAAGAAAAGAGCTC	3194

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      11 RESULT
US-08-713-118-1
: Sequence 1, Application US/08713118
: Patent No. 6040436
: GENERAL INFORMATION:
: APPLICANT: Franco, Rodrigo
: APPLICANT: Sun Chen, Ai Ru
: APPLICANT: Suey, David J.
: TITLE OF INVENTION: NOCLETIC ACID ENCODING HUMAN NEURONAL
: TITLE OF INVENTION: CALCION CHANNEL SUBUNITS
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
: STREET: Two Millitia Drive
: CITY: Lexington
: STATE: MA
: COUNTRY: USA
: ZIP: 02173-4799
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/713.118
: FILING DATE: 16-SEP-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Mata, Elizabeth W.
: REGISTRATION NUMBER: 38,236
: REFERENCE/DOCKET NUMBER: ACC96-01
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-861-9540
: TELEFAX: 617-861-6240
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 7266 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 92..7102
US-08-713-118-1

Query Match 2.9%; Score 46.6; DB 3; Length 7266;
Best Local Similarity 46.7%; Pred. No. 0.16;
Matches 209; Conservative 0; Mismatches 237; Indels 2; Gaps 2.

oy 855 ggaacagcccccttgagacagctcgatantctaacggttgagaccacagcgaagagag 914
db 2696 ggaagagcccccaagccgagagccggagagcccggtcccgagagacgacgacgacgacg 2755

```

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OY 915 aaattctcccaatgctcatcgtcaacagagaaactgcagcgccctggcccaaggcgccg 974
DB 2756 CACCCGACGACACAGCAAGAGAGCGCCGCGGGGCCCGGAGAGCGAGCGCGCGCA 2815
OY 975 tcggagacagcgccgcaagtcctcccaaggcgcccgcccgaaacgcagtcagcccgagc 1034
DB 2816 CCCCCAGCCCGGAGCGCGCGCGCGCGCGCACCGCGCGCGCTCCCGGAGAGCGCGCC 2875
OY 1035 tcggagacgctccgagangtcggcgccctggcgcgagaaagaggttcagtcggagaccgag 1094
DB 2876 CAGCCCGACGACCCCGACCGCACCGCGCACCGAGATCCAGACAGAGTGCGCC 2935
OY 1095 gacgcgctgggtgtgtctgacacggcgagccattctcgtcagaagaagagagcgctgcg 1153
DB 2936 GCGCGCCAGAGGCGAGCGCGCGCGCGCGCACCGCGCGCGCGCGCGCGCGCGCGGAG 2995
OY 1154 gcggtgagcccgagagagagagcgctgtgtacagcagagtcacgctgcagcgcttcgct 1213
DB 2996 CCGGAGAGCGCGGAGAGCGCGCGCGCGCGCACCGCGCGCGCGCGCGCGCGCGCT 3055
OY 1214 gctggagagcaaaagagaaagtgctcagagctggagcgatgagtgagagaaagaaagaa 1273
DB 3056 -CACGAGCGCTGTGGAGAAAGACACACGAGAGAGAGGCGCACGAGAGAGAGCTGAGAT 3114
OY 1274 ggtggagagcgaggtcgaaatgaggtc 1301
DB 3115 AGTGGAGCGGACAGAAAGAAAGAGAGCTC 3142

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RESULT 12  
US-09-452-007-1  
Sequence 1, Application US/09452007  
Patent No. 6140485

## GENERAL INFORMATION:

APPLICANT: Franco, Rodrigo  
APPLICANT: Sun Chen, Ai Ru  
TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL  
TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Milltia Drive  
CITY: Lexington  
STATE: MA

COUNTRY: USA  
ZIP: 02173-4799

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/452,007

## FILING DATE:

## CLASSIFICATION:

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/713,118  
FILING DATE: 16-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Maia, Elizabeth W.  
REGISTRATION NUMBER: 38,236  
REFERENCE/DOCKET NUMBER: ACC96-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540

## INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 7266 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 92..7102  
US-09-452-007-1

Query Match 2.9%; Score 46.6; DB 4; Length 7266;  
Best Local Similarity 46.7%; Pred. No. 0.16;  
Matches 209; Conservative 0; Mismatches 237; Indels 2; Gaps 2;

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OY 855 ggaacgcccgcgtgtgagacagctcgatantcaacgctgtgaccacagagagagag 914
DB 2696 GCAGAGCGCCCGCAAGAGCGAGAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 2755
OY 915 aaattctcccaatgctcatcgtcaacagagaaactgcagcgccctggcccaaggcgccg 974
DB 2756 CACCCGACGACACAGCAAGAGAGCGCCGCGGGGCCCGGAGAGCGAGCGCGCGCGCA 2815
OY 975 tcggagacagcgccgcaagtcctcccaaggcgcccgcccgaaacgcagtcagcccgagc 1034
DB 2816 CAGCCCGACGACCCCGACCGCACCGCGCACCGAGATCCAGACAGAGTGCGCC 2875
OY 1035 tcggagacgctccgagangtcggcgccctggcgcgagaaagaggttcagtcggagaccgag 1094
DB 2876 CAGCCCGACGACCCCGACCGCACCGCGCACCGAGATCCAGACAGAGAGTGCGCC 2935
OY 1095 gacgcgctgggtgtgtctgacacggcgagccattctcgtcagaagaagagagcgctgcg 1153
DB 2936 GCGCGCCAGAGGCGAGCGCGCGCGCGCGCACCGCGCGCGCGCGCGCGCGCGCT 3055
OY 1154 gcggtgagcccgagagagagagcgctgtgtacagcagagtcacgctgcagcgcttcgct 1213
DB 2996 GCGGAGAGCGGAGAGAGCGCGCGCGCGCGCACCGCGCGCGCGCGCGCGCGCGCT 3055
OY 1214 gctggagagcaaaagagaaagtgctcagagctggagcgatgagtgagagaaagaaagaa 1273
DB 3056 -CACGAGCGCTGTGGAGAAAGACACACGAGAGAGAGGCGCACGAGAGAGAGCTGAGAT 3114
OY 1274 ggtggagagcgaggtcgaaatgaggtc 1301
DB 3115 AGTGGAGCGGACAGAAAGAAAGAGAGCTC 3142

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RESULT 13  
US-08-455-543A-7

Sequence 7, Application US/08455543A  
Patent No. 5792846

## GENERAL INFORMATION:

APPLICANT: Harpold, Michael  
APPLICANT: Ellis, Steven  
APPLICANT: Williams, Mark  
APPLICANT: Feldman, Daniel  
APPLICANT: McCue, Ann  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,543A  
FILING DATE: May 31, 1995

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2  APPLICATION NUMBER: 08/223,305
3  FILING DATE: April 4, 1994
4  PRIOR APPLICATION DATA:
5  APPLICATION NUMBER: 07/868,354
6  FILING DATE: April 10, 1992
7  PRIOR APPLICATION DATA:
8  APPLICATION NUMBER: US 07/745,206
9  FILING DATE: 15-AUG-1991
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: US 07/620,250
12 FILING DATE: 30-NOV-1990
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: US 07/482,384
15 FILING DATE: 20-FEB-1990
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER: US 07/603,751
18 FILING DATE: 04-APR-1989
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: WO PCT/US89/01408
21 FILING DATE: 04-APR-1989
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: US 07/176,899
24 FILING DATE: 04-APR-1988
25 ATTORNEY/AGENT INFORMATION:
26 NAME: Seidman, Stephanie L.
27 REGISTRATION NUMBER: 33,779
28 REFERENCE/DOCKET NUMBER: 6362-52517
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: (619)238-0999
31 TELEFAX: (619)238-0062
32 INFORMATION FOR SEQ ID NO: 7:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 7362 base pairs
35 TYPE: nucleic acid
36 STRANDEDNESS: double
37 TOPOLOGY: linear
38 MOLECULE TYPE: DNA (genomic)
39 FEATURE:
40 NAME/KEY: CDS
41 LOCATION: 144..7163
42 FEATURE:
43 NAME/KEY: 5'UTR
44 LOCATION: 1..143
45 FEATURE:
46 NAME/KEY: 3'UTR
47 LOCATION: 7161..7362
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      FILING DATE: 20-FEB-1990
      PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US 07/603,751
        FILING DATE: 04-APR-1989
        PRIOR APPLICATION DATA:
          APPLICATION NUMBER: WO PCT/US89/01408
          FILING DATE: 04-APR-1989
          PRIOR APPLICATION DATA:
            APPLICATION NUMBER: US 07/176,899
            FILING DATE: 04-APR-1988
            ATTORNEY/AGENT INFORMATION:
              NAME: Seidman, Stephanie L.
              REGISTRATION NUMBER: 33,779
              REFERENCE/DOCKET NUMBER: 6302-52517
            TELECOMMUNICATION INFORMATION:
              TELEPHONE: (619)238-0999
              TELEFAX: (619)238-0062
            INFORMATION FOR SEQ ID NO: 7:
              SEQUENCE CHARACTERISTICS:
                LENGTH: 7362 base pairs
                TYPE: nucleic acid
                STRANDEDNESS: double
                TOPOLOGY: linear
              MOLECULE TYPE: DNA (genomic)
              FEATURE:
                NAME/KEY: CDS
                LOCATION: 144..7163
              FEATURE:
                NAME/KEY: 5'UTR
                LOCATION: 1..143
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Query Match             2.9%; Score 46.6; DB 1; Length 7362;
Best Local Similarity   46.7%; Pred. No. 0.16;
Matches 209; Conservative 0; Mismatches 237; Indels 2; Gaps 2.

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      Oy 915 aaattctccagatgtcatgtcaagaaagtaactgcagcgcgcgcttgcgccagcgcg 974
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Db 2988 GGCGCAAGGCGAGCGCGCGCGCGCGAGCACCGCGCGCGGCCCCCGAGCGGGGGCCCCGGAG 3047

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Db 3108 -CACGAGGCTGTGGAGAGACGACGAGAGAGAGGCCACGAGAGAGAGGCTGAGAT 3166  
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Search completed: June 28, 2001, 20:25:17  
Job time: 5605 sec



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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.



REFERENCE.	Methods Enzymol. 303, 19-44 (1999)
AUTHORS	2 (sites)
TITLE	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	20499374
REFERENCE	3 (sites)
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoaka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsuami,T., Tashiro,H., Itoh,M., Kikuchi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishio,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Onata,E., Matsuhiki,M., Tameda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Okazaki,Y., Muramatsu,M., Inoue,Y. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipicillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
REFERENCE	4 (sites)
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and FANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409, 685-690 (2001)
REFERENCE	5 (bases 1 to 2374)
AUTHORS	Aachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakawa,T., Carninci,P., Fukuda,S., Furukoshi,Y., Furuno,M., Hanakawa,T., Hara,A., Hayatsu,N., Hiramoto,K., Hirooka,T., Horii,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,Y., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE	Direct Submission
JOURNAL	Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT	Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and genome science laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to









[illegible]

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QY	816	-agccccgccccccactccacgtctctgctgcgcgcgctgagacagccccg-c-tggagac	873
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Db	599	ATCGACAA-GAGGAATGCAAGAGCGCTGGCCAGCGCAGAGAGCAGAGGAGAACCA	657
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ACCESSION	FACTOR RECEPTOR KINASE SUBSTRATE. ; mRNA sequence.					
VERSION	AA411593					
KEYWORDS	EST..					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS	1 (bases 1 to 558) Hillier,L., Allen,M., Bowles,L., Dubucque,T., Gaisel,G., Jost,S., Kueba,T., lacy,M., Le'N., Lennon,G., Marra,N., Martin,J., Moore,B., Schellenberg,K., Stepien,M., Tan,F., Theising,B., White,Y., Wyllie,T., Meterston,R. and Wilson,R.					
TITLE	WashU-Merck EST Project 1997					
JOURNAL	Unpublished (1997)					
COMMENT	Contact: Wilson RK Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LBNL ; contact the IMAGE Consortium ( <a href="mailto:infoimage.lbnl.gov">infoimage.lbnl.gov</a> ) for further information. Possible reversed clone; similarity on wrong strand Seq primer: ~28ml3 rev2 ET from Amersham High quality sequence stop: 465. Location/Qualifiers 1..558 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:755196" /clone_lib="Soares ovary tumor NBHOT" /sex="Female" /tissue_type="Ovarian tumor" /lab_host="DH10B (ampicillin resistant)" /note="Organ: ovary; Vector: pUT3D (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I- oligo(dT) primer [5 TGTTACCATCTGAGTGCGAGCCGGGTGTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pUT3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaalido."					
FEATURES						
SOURCE						
BASE COUNT	95 a 194 c 144 g 125 t					
ORIGIN						
Query Match	31.2%; Score 510.8; DB 7; Length 558;					
Best Local Similarity	98.0%; Pred.No.2.e-102;					
Matches 548;	Conservative 0; Mismatches 8; Indels 3; Gaps 3;					
OY	1062	ctgcagagcaaggcgttaagtctcggaacgcttgacgcgcttggtgtgctgaccggggcg	1121			
Db	558	CTGCAGGCCCAAGGGCTTAGCTCCGGGACCGCGACGCGCTGGTGTGACCGGGC	499			
OY	1122	ca-cttttcgcgtcagaagaggagcgtcgcgcggtgtagcccgagaggggcact	1180			
Db	498	CAGCTTTCCTGCTCTACAAGAAGAGAGACTGCGCGCGGTGAGCCCCGAGAGGGGACACT	439			
OY	1181	gtgtacagcagatcacgcgtgacgcgttcgctgtgtgagagcaaaagaaigtgcaga	1240			
Db	438	GTTGACACCCCAAGGTCACCGATCAGCGC--TCGCTGCTGGAGCAAAAGAAAGTGTCA	380			
OY	1241	gctgagagccaattgatgtgaggaagcaaaa-gaagaaggtggaagcgaggtggaatatgaggg	1299			
Db	379	GCTGGAGGCAGTGAATGAGAAAGCAAAGCAAAAGTGAACGCAAGGTGCAAAATGGAGG	320			
OY	1300	tcaattgcacctccgcggcccttcgcaaaaggttacagagcccgttgtgaaacaggact	1359			
Db	319	TCATTGTGACTGCGCAGGGGCCCTTTCGCAAAAGTAGTACAGAGCCCGGTGGAGAACAGACT	260			
OY	1360	cctcagactctccccaatagcgaagtcatctcttcgtgaagatgagccaattgctccgac	1419			

DB	259	CCTCAGACCTCTCCCAATGACGGAGTGCATCTTCTGAAGATGGCCAACTGCTCCGGC	200
QY	1420	cctggtcttccccaatcccggtggaagaacttaacgactctgtctgcagtcctcccgag	1479
DB	199	CTGTGCTCTTCCCAATCCCGGTGAGACAGACTTAAGATCCTTGTGCACTCTCCGAG	140
QY	1480	aggaatctgacgtctgtgagatgaggagagggctggaagaactctcaggaagaagcgctaca	1539
DB	139	AGGATCTGGACTGCGTGGAGATGGGAGAGCGCTGGAGACAGTCTACGGAAACGCTTACGA	80
QY	1540	gaaccccgagagaggtgcagtgtagagccctgagcattgtataatgctggccagcctaatac	1599
DB	79	GACCCCCGAGAGAGGCTGAGTGGAGCCCTGAGCATTTGTAATATGTGCGCCAGCTATTAAC	20
Db	19	AGCTTCGCTGCTTACCAAA	1
RESULT	10		
LOCUS	A1582188		
DEFINITION	A1582188	518 bp mRNA EST	14-DEC-1999
ACCESSION	A1582188	tg3ed6.x1 NCI_CGAP.Lu19 Homo sapiens CDNA clone IMAGE:2213506	3'
VERSION	A1582188	similar to SW:EP58.MOUSE Q08509 EPIDERMAL GROWTH FACTOR RECEPTOR	
KEYWORDS	A1582188.1	GI:4568085	
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
TITLE	NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
COMMENT	Tumor Gene Index		
	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-remail.nih.gov		
	Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.		
	Emmert-Buck, M.D., Ph.D.		
	CDNA Library Preparation: M. Bento Soares, Ph.D.		
	CDNA Library Arrayed by: Greg Lennon, Ph.D.		
	DNA Sequencing by: Washington University Genome Sequencing Center		
	Clone distribution: NCI_CGAP clone distribution information can be		
	found through the I.M.A.G.E. Consortium/INMIL at:		
	www-bio.llnl.gov/bdrrp/image/image.html		
	Insert length: 1475 Std Error: 0.00		
	Seq primer: -40UP from Glibco		
	High quality sequence stop: 461		
	POLYA-No.		
FEATURES			
SOURCE			
	Location/Qualifiers		
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	/db_xref="taxon:9606"		
	/clone="IMAGE:2213506"		
	/clone_id="NCI_CGAP.Lu19"		
	/tissue_type="squamous cell carcinoma, poorly		
	differentiated (4 pooled tumors, including primary and		
	metastatic)"		
	/dev_stage="adult"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: Lung; Vector: pT7TD-Pac (Pharmacia) with a		
	modified polylinker; 1st strand cDNA was prepared from		
	pooled lung tumor tissue, and was then primed with a Not I		
	- oligo(dT) primer. Double-stranded cDNA was ligated to		
	Eco RI adaptors (Pharmacia), digested with Not I and		
	cloned into the Not I and Eco RI sites of the modified		
	pT73 vector. Library went through one round of		
	normalization. Library constructed by Bento Soares and M.		
	Fatima Bonaldo."		
BASE COUNT	112 a	162 c	170 g
	74 t		



**ORIGIN**

Query Match	30.68;	Score 499.6;	DB 22;	Length 518;
PostgreSQL similarity	08.88;	Word No. 5	30-100;	

Matches 5.14; Conservative 0; Mismatches 4; Indels 2; Gaps 1;

Matches 514; Conservative 0; Mismatches 4; Indels 2; Gaps 1;

Oy	262	ggaatcccgctggcgcctgcctgcgagagcaaaagctcaatcccaagctgaanaacagactctcgagactc	321
Db	1	GGATCCCGTGGCGCTGCTGGCGGGACAAACGTATCACTCCACGTGAATAACGAGCTCTGGACCTC	60
Oy	322	gctcgaggagactcgttggaaaccgcgcccgagcttgagactgtgtccccgagaggaggaaccaccata	381
Db	61	GCTGGCGGACATCTGTGGACACCCCGCGGGCTGGACCTCTCCCGGAGGAGGACCCCATTA	120
Oy	382	cagaaaccgaagctctctcaagcgccttgagagccgcgctcaactgaaccgcgagagccgcgcctg	441
Db	121	CAGAACCCAGTCTTTCACCGGGCTGGACCCCGGCTACTGTACCCCGAGACCCCGCGCTG	180
Oy	442	ggaggaaccagctctgagaanaacagctacaagcacgagcggagagcgcccgagcaaaagcgccc	501
Db	181	GGAGGACCCCACTTGAAGAAACGCTACAGCAGACGACGGGAGGCGCGCGGCAAGAGCGCCCC	240
Oy	502	cgaaagctgccttcaaatgttcaaccgaagaaactggagagccaaatctgaagccctcaagcttgag	561
Db	241	CCAGGTCCTCTCAATAGTGTCAACCAG - - ACTTGGAGCCAGAACTTGAAGCTTCACCTTGAG	298
Oy	562	tcaagaaacagacaggaanaatgggtctctgtgtaatatgaactccaagcgcgcgcaaacagcagt	621
Db	299	TCACAGACACAGCAAAAAATCGCTCTCTGTGAATTATGACTTCCAGCGCCCAACAGCAGT	358
Oy	622	gagagctgcgttcaagacagccgagaaacgtactgtgaagttcctgatagaacatctgaagtgtg	681
Db	359	GAGCTGTGTGTAAACACACGGGAGAGTATGGAGGTCCTGGATGCACTCGTAAGTGGTG	418
Oy	682	aaaggtctggagaccagcgaggcagagaggaatagtgtccctatacaacatcctgaacccctac	741
Db	419	AAGCTTCCGGACCAACAGCGCGGACAGAGGAAATGTGCCCTTACAAACATCTGACACCTTAC	478
Oy	742	cccggaaccgcgcttgacacacacagacaaagcccttgccgca	781
Db	479	CCCGGACCCCGGCTGCACCAACAGCCAAAGCCCTCTCCCGCA	518

RESULT 11

LOCUS	BF974720	1009 bp	mRNA	EST	22-JAN-2001
DEFINITION	602245363F1	NIH_MGC_48	Homo sapiens cDNA clone	IMAGE:4336694	5

main sequence.  
ACCESSION BF974720

<b>KEYWORDS</b>	<b>EST.</b>
<b>SOURCE</b>	human.

Chromatium  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi  
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 REFERENCE  
 1 (bases 1 to 1009)

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4336694"
/clone_1lb="NIH_MGC_48"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/name="Organ: B-cells; Vector: pOT87; Site: 1: XhoI;
Site: 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAC(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

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Query Match	30.5%	Score 498.8	DB 172	Length 1009
Best Local Similarity	94.7%	Pred. No. 1e-99		
Matches 551; Conservative	0	Mismatches 24	Indels 9	Gaps 7

QY	532	tggagagccagaatcctgtgagcctcagctggagatccagagacagcggaaaaatgggtccctgtc	591
Db	143	tttcgagccagaaatctgacccctcagctggagtcagagacagcggaaaaatgggtccctgtc	202

QY 592 aattatgacttcagggccgcgaacacagcagtgagctgtcgtccaagcagcgggacgtactg 651

Db 203 AATTATGACTTCCAGGCCCGCAACAGCAGTGAGCTGTCGGTCAAGCAGCGGGACGTACTG 262

QY	652	gaggtcctcgtgattgaaacatgctcgtaaagtggtggaaggtctcggaaaccacgagcgaggcagaagagga	711
DB	263	GAGGTCTCTGGATGAGACAGTCGTAAAGTGGTGGAAGGTTCCGAGACCCAGCGGAGGAGAGGGA	322
QY	712	tatgtgccttaaacatctctgtacacccctaccccgagacccggtctgcacacagcccaagc	771
DB	323	TATGTGCCCTTACCAATCCTTGACACCCCTAACCCCGAGACCCCGGCTGCACACAGCCAAAGC	382
QY	772	cctgtcccgagccttgaagaacatctctctctcacaccacagccccagccccggccccacct	831
DB	383	CCGTGCCCGAGCCTTAACAGCAGCAGCTCTCTCTCCACACACAGCCCGCCCGCCCACT	442
QY	832	ccagctctcgtcctcgcccccgctcgagacagcccccgctctggacagctctgata - nctcaac	890
DB	443	CCAGCTCTGTGGCTCGGCCCCCGCTGGGACAGGCCCGCCTGGAGACAGCTGGGATAGCTTCAAC	502
QY	891	ggctctggagccccaagcagagaaagagaatctctccagatgctcatcgtcaacagaggaactg	950
DB	503	GGCTTTGGACCCCGAGGAGAGAGAAATTTCTCCAGATGCTCATGTGTAACACAGGAATCG	562
QY	951	cagagcgagccttgccacagag - cgcgtctggagacgagacgagtcaccaaagccccgcgc	1009
DB	563	CAGGCGCGCGCTTGCCCAAGGCCCGCGTCCGAGACGAGCCCGCAGTCCCAAGGCCGCCCGC	622
QY	1010	cccggaacccgcaagctcagcccgagctctggaaegctccgagntccgagctcgtgctgcaagn	1069
DB	623	CCCGGAACCGCAGCTCAG - CCGGGGCTCGGAGCCCTCCAGAGTCCCGCGCTGCTCACAAG -	680
QY	1070	caagagcttgaactccggagacccgttgaaacgcgtctggtcttgctgacaggggcgcactcttc	1129
DB	681	CAAGGCGCTTACCTCCGAGACCTGACGCGC --- TGGTGTGCTGA - CGGGGCCCGACCTTTC	736
QY	1130	tcgctgcagaagaagaagctgcgg	1153
DB	737	TCGAGAAAGAGGACCTTGGC	759

FEATURES	http://image.llnl.gov	RESULT	12
source	Plate: L1CM1209 row: m column: 15		BE543227
	High quality sequence stop: 735.		LOCUS
	Location/Qualifiers		BE543227 596 bp mRNA
	1. .1009		DEFINITION
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			mRNA sequence.

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ACCESSION    BE543227
VERSION      BE543227.1
KEYWORDS     GI:9771872
SOURCE       human.
ORGANISM     Homo sapiens
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              Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE    1 (bases 1 to 596)
              NIH-MGC http://mgc.nci.nih.gov/.
              National Institutes of Health, Mammalian Gene Collection (MGC)
              JOURNAL
              COMMENT
              Email: cgapbs-remail.nih.gov
              Tissue Procurement: ATCC
              CDNA Library Preparation: Life Technologies, Inc.
              DNA Library Arrayed by: Incyte Genomics, Inc.
              DNA sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LNL at:
              http://image.llnl.gov
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              Location/Qualifiers
                1..596
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                /lab_host="DH10B"
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                Site_2: SalI; Cloned unidirectionally. Primer: oligo dt.
                Average insert size 1.4 kb. Library prepared by Life
                Technologies."
BASE COUNT    115 a      205 c      195 g      81 t
ORIGIN
Query Match      30.5%; Score 498.6; DB 136; Length 596;
Best Local Similarity 96.0%; Pred. No. 1,1e-99;
Matches 574; Conservative 0; Mismatches 17; Indels 7; Gaps 6;

OY 582 ggtctgtatattatgactccagccggaacagcgtgactgtgtcgaagcgcg 641
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Db 1 ggtctgtatattatgactccagccggaacagcgtgactgtgtcgaagcgcg 60

OY 642 ggaactgagaggttcctgtgagtgacgtcgaagtggtgtgagaggttcgagaccagcg 701
    |||||||
Db 61 ggaactgagaggttcctgtgagtgacgtcgaagtggtgtgagaggttcgagaccagcg 120

OY 702 gcaagagagagatgtgcctcacaacatctgacacctaccgccggaaccggctgacaca 761
    |||||||
Db 121 gcaagagagagatgtgcctcacaacatctgacacctaccgccggaaccggctgacaca 180

OY 762 cagcacaagacctctccgcaagcctgaaacagacatcctctccacaacagccagccccc 821
    |||||||
Db 181 cagcacaagacctctccgcaagcctgaaacagacatcctctccacaacagccagccccc 240

OY 822 ggcacacacacacacacacacacacacacacacacacacacacacacacacacacacac 881
    |||||||
Db 241 ggcacacacacacacacacacacacacacacacacacacacacacacacacacacacac 299

OY 882 ta-nctcaagagcgtgagaccccaagagaagaattctccagatgcatcgtcaaa 940
    |||||||
Db 300 TAGCCTAACGGCTTGGACCCCAAGAGAGAGAAATTTCCAGATGCTCATCTGTCAA 359

OY 941 cgaagaaactcgaagcgc-gcctgtgccagagcgctcggagacagcgagcgcaat-ccca 998
    |||||||
Db 360 CGAGGAACCTGCAAGCGCAAGCTTGGCCCAAGGCGCTCGGGACCAAGCGCGCAATACCCA 419

OY 999 gggcccgccgcccggagacgcgtcagccggcgtcggagcgtcctcgagntcgcg-9 1056
    |||||||
Db 420 GGCCCGAGAGCCCGGAAACCGCAATCAGCCCGGGCTCGAGACGCTCTCGAAGTCCGACG 479

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OY 1057 cctgctgcagagcaaggccttagctccgggaaccgtgacgcgtgtgtcgaagc 1116
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Db 480 CTGGCGTCAGAGCCCAAGGCGCTTACTCCGGGACCGGTGAGCGCGTGTGTCGACGCG 539

OY 1117 gggcgacattctctcgtcgcagaagagagcgtcggcggtgagcccgagaggg 1174
    |||||||
Db 540 GGGCGCAAGTTACTCTCGTCGACAGAGGAGACGCTG-GGGCGGTGAGCCCGCAAGAGCG 596

RESULT 13
LOCUS      A1183328/c
DEFINITION A1183328 542 bp mRNA EST 28-OCT-1998
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            GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EP58. [1]; mRNA sequence.
ACCESSION  A1183328
VERSION     A1183328.1
KEYWORDS    GI:3733966
SOURCE      EST.
ORGANISM    Homo sapiens
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              Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE    1 (bases 1 to 542)
              NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
              National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
              JOURNAL
              COMMENT
              Email: cgapbs-remail.nih.gov
              This clone is available royalty-free through LNL; contact the
              IMAGE Consortium (info@image.llnl.gov) for further information.
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                /note="Organ: placenta; Vector: pT73D (Pharmacia) with a
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                strand cDNA was primed with a Not I - oligo(dT) primer [5'
                TCTTACCAATCTGAAGTGGAGCGCGCGCGCATTTTCTTTTCTTTT 3'],
                double-stranded cDNA was size selected, ligated to Eco RI
                adapters (Pharmacia), digested with Not I and cloned into
                the Not I and Eco RI sites of a modified pT73 vector
                (Pharmacia). Library constructed by Bento Soares and
                M.Fatima Bonaldi."
BASE COUNT    93 a      191 c      136 g      117 t      5 others
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Query Match      30.0%; Score 489.8; DB 17; Length 542;
Best Local Similarity 94.8%; Pred. No. 9,1e-98;
Matches 514; Conservative 0; Mismatches 27; Indels 1; Gaps 1;

OY 1074 ggtcttagctccggagcgtgagcgcgtgtgtgtcgtgacccggcgaca-ctttctcg 1132
    |||||||
Db 542 GGTCTTAGCTCCGGGACCGTGGAGCGCGNNNGTGTGCTGACGGGGCGCAGCTTTCTCG 483

OY 1133 ctgcagaagaagagagcgtcggtgagcccgagagagggcgacgtgtgtcagcagcag 1192
    |||||||
Db 482 CTGCAGAGAGAGAGAGCGTCCGCGGCGGTAGCCCAAGGAGGGGCGACCTGTGTACAGCCA 423

OY 1193 gtacacgtgacgcgttcgtcgtgtgagagacaagaagtgatcaagcttgagagcagt 1252
    |||||||
Db 422 GTACACGTGACGCGCTTCGCTGCTGAGACACAAAAGAGAAAGTGTCAAGCTGCAAGCAGT 363

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